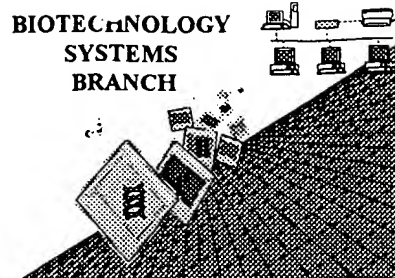


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/857,372

Source: PL 09

Date Processed by STIC: 6/26/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/857,372

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 (NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
 (NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
 Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
 "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

PCT09

RAW SEQUENCE LISTING

DATE: 06/26/2001

PATENT APPLICATION: US/09/857,372

TIME: 08:53:19

Input Set : A:\JAB-1430.txt

Output Set: N:\CRF3\06262001\I857372.raw

Does Not Comply
Corrected Diskette Needed
see pp 2-5

3 <110> APPLICANT: Contreras, Roland
4 Nelissen, Bart
5 DeBacker, Marianne
6 Luyten, Walter
7 Viaene, Jasmine
8 Logghe, Marc
10 <120> TITLE OF INVENTION: Drug Targets in Candida Albicans
12 <130> FILE REFERENCE: 53731/000
OK 14 <140> CURRENT APPLICATION NUMBER: US/09/857,372
15 <141> CURRENT FILING DATE: 2001-06-04
17 <150> PRIOR APPLICATION NUMBER: 982204122.0
18 <151> PRIOR FILING DATE: 1998-12-04
E--> 20 <160> NUMBER OF SEQ ID NOS: *2022 (next pages)*
22 <170> SOFTWARE: PatentIn Ver. 2.0 *pp 2-4*

ERRORED SEQUENCES

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161 <211> LENGTH: 619
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163 <213> ORGANISM: Candida albicans
165 <400> SEQUENCE: 6
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E--> 175 tatccattgt accaattggt aaaacatttt gttagttttt tgttactagt ataaaaannat 600
E--> 176 aataaaagtt tttttcaac 619
236 <210> SEQ ID NO: 9
237 <211> LENGTH: 119
238 <212> TYPE: DNA
239 <213> ORGANISM: Candida albicans
241 <400> SEQUENCE: 9
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243 tagttggtat aatgatttat gtattatctt aattcattat tattagtttc ggtcacaaa 119

*see item 9 on
Err
summary sheet*

09/857,372 2

<400> 22 *last sequence in file*

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*see p. 5
for more
info*

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09/857,372 4

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insert a hard return after *h* response 09/857,372-5

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same env

<400> 19

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<220>

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same

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/857,372

DATE: 06/26/2001

TIME: 08:53:20

Input Set : A:\JAB-1430.txt

Output Set: N:\CRF3\06262001\I857372.raw

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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:175 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
M:340 Repeated in SeqNo=6
L:242 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
L:770 M:282 W: Numeric Field Identifier Missing, <211> is required.
L:770 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:770 M:282 W: Numeric Field Identifier Missing, <213> is required.
L:775 M:283 W: Missing Blank Line separator, <220> field identifier
L:778 M:282 W: Numeric Field Identifier Missing, <211> is required.
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L:787 M:282 W: Numeric Field Identifier Missing, <213> is required.
L:20 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (20) Counted (22)